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FIG. 1A

| | | |
|-----|---|-----|
| 1 | TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGTTGGGGAGCC | 60 |
| 61 | TCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGATAGGGCGAGGCT | 120 |
| 121 | GTGCTGTCCTTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGG | 180 |
| 1 | M A S S I L K W V V | 10 |
| 181 | TCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGGGAGGAGG | 240 |
| 11 | S H Q S C S R S S R S K P R D Q R E E A | 30 |
| 241 | CCGGGAGCAGCGACCTGAGCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGG | 300 |
| 31 | G S S D L S S R Q D A E N A E A K L R G | 50 |
| 301 | GCCTCCCGGGGCAGCTTGTGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGC | 360 |
| 51 | L P G Q L V D I A C K V C Q A Y L G Q L | 70 |
| 361 | TGGAGCATGAGGACATCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGT | 420 |
| 71 | E H E D I D T S A D A V E D L T E A E W | 90 |
| 421 | GGGAGGACCTGACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATT | 480 |
| 91 | E D L T Q Q Y Y S L V H G D A F I S N S | 110 |
| 481 | CAAGAAATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC | 540 |
| 111 | R N Y F S Q C Q A L L N R I T S V N P Q | 130 |
| 541 | AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGG | 600 |
| 131 | T D I D G L R N I W I I K P A A K S R G | 150 |
| 601 | GCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACC | 660 |
| 151 | R D I V E M D R V E E I L E L A A A D H | 170 |
| 661 | ACCCTCTTTCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCA | 720 |
| 171 | P L S R D N K W V V Q K Y I E T P L L I | 190 |
| 721 | TCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGA | 780 |
| 191 | C D T K F D I R Q W F L V T D W N P L T | 210 |
| 781 | CCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACA | 840 |
| 211 | I W F Y K E S Y L R F S T Q R F S L D K | 230 |

2/24

FIG. 1B

| | | |
|------|---|------|
| 841 | AGCTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATG | 900 |
| 231 | <u>L D S A I H L C N N A V Q K Y L K N D V</u> | 250 |
| 901 | TGGGCCGCGAGCCCCCTGCTGCCCCGACACAACATGTGGACCAGCACCAGGTTCCAGGAGT | 960 |
| 251 | <u>G R S P L L P A H N M W T S T R F Q E Y</u> | 270 |
| 961 | ACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGA | 1020 |
| 271 | <u>L Q R Q G R G A V W G S V I Y P S M K K</u> | 290 |
| 1021 | AGGCCATCGCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCT | 1080 |
| 291 | <u>A I A H A M K V A Q D H V E P R K N S F</u> | 310 |
| 1081 | TTGAGCTCTACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGA | 1140 |
| 311 | <u>E L Y G A D F V L G R D F R P W L I E I</u> | 330 |
| 1141 | TCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGG | 1200 |
| 331 | <u>N S S P T M H P S T P V T A Q L C A Q V</u> | 350 |
| 1201 | TGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGC | 1260 |
| 351 | <u>Q E D T I K V A V D R S C D I G N F E L</u> | 370 |
| 1261 | TCCTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCATTTCAGCGGGTCCGACCTCTGCGTGG | 1320 |
| 371 | <u>L W R Q P V V E P P P F S G S D L C V A</u> | 390 |
| 1321 | CGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCCTCTGCAACCTCAAGGCCT | 1380 |
| 391 | <u>G V S V R R A R R Q V L P V C N L K A S</u> | 410 |
| 1381 | CGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCCTCGGCCATGCCAGACC | 1440 |
| 411 | <u>A S L L D A Q P L K A R G P S A M P D P</u> | 430 |
| 1441 | CTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGG | 1500 |
| 431 | <u>A Q G P P S P A L Q R D L G L K E E K G</u> | 450 |
| 1501 | GGCTCCCCCTGGCCTTGCTGGCACCCCTTAAGGGGGGCGAGAGCGGTGGAGCCGCAC | 1560 |
| 451 | <u>L P L A L L A P L R G A A E S G G A A Q</u> | 470 |
| 1561 | AGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTGCCCACG | 1620 |
| 471 | <u>P T R T K A A G K V E L P A C P C R H V</u> | 490 |
| 1621 | TGGACAGTCAGGCCCCAAACACCGGTGTCCCGTAGCCCAGCCGCCAAAGCTGGGATC | 1680 |
| 491 | <u>D S Q A P N T G V P V A Q P A K S W D P</u> | 510 |

3/24

FIG. 1C

1681 CAAACCAGCTAAATGCGCACCCGCTGGAGCCTGTGCTGCGGGGCCTGAAGACAGCAGAGG 1740
511 N Q L N A H P L E P V L R G L K T A E G 530

1741 GCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCA 1800
531 A L R P P P G G K G S 541

1801 GGAGTACAGGTTGCAGCCACTCTCCCAAGGGCGAATTC 1838

4/24

FIG. 2

| | | |
|-----|--|-----|
| 1 | ATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCCGAGAC | 60 |
| 1 | I D G L R N I W I I K P A A K S R G R D | 20 |
| 61 | ATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCTCTT | 120 |
| 21 | I V C M D R V E E I L E L A A A D H P L | 40 |
| 121 | TCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGAC | 180 |
| 41 | S R D N K W V V Q K Y I E T P L L I C D | 60 |
| 181 | ACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCTGACCATCTGG | 240 |
| 61 | T K F D I R Q W F L V T D W N P L T I W | 80 |
| 241 | TTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGAC | 300 |
| 81 | F Y K E S Y L R F S T Q R F S L D K L D | 100 |
| 301 | AGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGC | 360 |
| 101 | S A I H L C N N A V Q K Y L K N D V G R | 120 |
| 361 | AGCCCCCTGCTGCCCCGACACAACATGTGGACCAGCACCAGGTTCAGGAGTACCTGCAG | 420 |
| 121 | S P L L P A H N M W T S T R F Q E Y L Q | 140 |
| 421 | CGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATC | 480 |
| 141 | R Q G R G A V W G S V I Y P S M K K A I | 160 |
| 481 | GCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTC | 540 |
| 161 | A H A M K V A Q D H V E P R K N S F E L | 180 |
| 541 | TACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCC | 600 |
| 181 | Y G A D F V L G R D F R P W L I E I N S | 200 |
| 601 | AGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAG | 660 |
| 201 | S P T M H P S T P V T A Q L C A Q V Q E | 220 |
| 661 | GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGG | 720 |
| 221 | D T I K V A V D R S C D I G N F E L L W | 240 |
| 721 | AGGCAG | 726 |
| 241 | R Q | 242 |

5/24

FIG. 3A

| | | | | |
|---------|-------|--------------------------------------|-----------------------------------|----------------|
| | | 1 | | 50 |
| BGS-42 | (1) | -----MASSILKWV | VSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAE | |
| TTL_PIG | (1) | MYTFVVRDENSSVYAEV | SRLLLATGHWKRLRRDNPRFNLMLGERNRLPFG | |
| TTLH_Hu | (1) | -----MAGKVKWV | TDIEKSVLINNFEKRGWVQVTENEDWNFYWMSV | |
| TTLH_Hu | (1) | ----- | ----- | |
| HOTTTL | (1) | ----- | ----- | |
| | | 51 | | 100 |
| BGS-42 | (43) | NAEAKLRGLPGQLVDIACKVCQAYLGQLEHEDIDTS | SADAVEDLTEAEWED | |
| TTL_PIG | (51) | RLGHEPGLMQLVNYRGADKLCRKASLVKLIKTSPEL | AESCTWFPESYVI | |
| TTLH_Hu | (42) | QTIRNVFSVEAGYRLSDDQIVNHFP--NHYELTRKD | LMVKN--IKRYRKE | |
| TTLH_Hu | (1) | ----- | MDIDKDL | LEAPLYLTPEGWSL |
| HOTTTL | (1) | ----- | ----- | |
| | | 101 | | 150 |
| BGS-42 | (93) | LTQQYYSIVHGDAFISNSRNYFSQCQALINRITS | VNPQTDIDGLRNIT | |
| TTL_PIG | (101) | YPTNLKTPVAPAQNGIHPPIHSSRTDEREFFLT | SYNKKKE-DGEGNVWIA | |
| TTLH_Hu | (88) | LEKEGSPLEAKDENGKYLDFVPVTYMIPADYNIF | VVEEFRKSPSSTWIM | |
| TTLH_Hu | (21) | FLQRYYYQVHEGAELRHLDTVQVRCEDILQQLO | AVVPQIDMEGDRNITWIV | |
| HOTTTL | (1) | ----- | MEGDRNEWIV | |
| | | 151 | | 200 |
| BGS-42 | (143) | KPAAKSRGRDIVCMDRVEEILELAAADHPLSRDN | -----KWVVQKYIETP | |
| TTL_PIG | (150) | KSSAGAKGEGILISSEATELLDFTDN | -----QGQ--VHVIQKYLERP | |
| TTLH_Hu | (138) | KPCGKAQKGIELINKLSQIKKWSRDSKTSSFVS | QSNKEAYVISLYINNP | |
| TTLH_Hu | (71) | KPGAASRGRGIMCMDHLEEMLKLVNCPVVMKDG | -----KWVVQKYIERP | |
| HOTTTL | (11) | KPGAASRGRGIMCMDHLEEMLKLVNCPVVMKDG | -----KWVVQKYIERP | |
| | | 201 | | 250 |
| BGS-42 | (188) | LLICD--TKFDLRQWFLVTDWNPLTIWFYKESYL | RFSTQRFSLDKLDSA- | |
| TTL_PIG | (190) | LLLEPGHRKFDIRSWVLVD--HOYNTLYREGVLR | TASEPYHTDNFODKT | |
| TTLH_Hu | (188) | LLIGG--RKFDLRLYVLVSTYRPLRCYMYKLGE | CRFCITVKYTPSTSELN | |
| TTLH_Hu | (116) | LLIFG--TKFDLRQWFLVTDWNPLTVWFYRDSY | IRFSTQPFSLKNLDS- | |
| HOTTTL | (56) | LLIFG--TKFDLRQWFLVTDWNPLTVWFYRDSY | IRFSTQPFSLKNLDS- | |
| | | 251 | | 300 |
| BGS-42 | (235) | --IHLCNNAVQKYLKNDVGRSPLLPAHNMWTS | TRFQEYLRQGRGAVWGS | |
| TTL_PIG | (238) | --CHITNHCIQKEYSKNYGKYE--E-GNEMF | FEFFNOYLTSAI-NITLES | |
| TTLH_Hu | (236) | MFVHLITNVAIQKHGEDYNHIH---G--GKW | TVSNLRLYLESTR-GKEVTS | |
| TTLH_Hu | (163) | --VHLCNNSIQKHLENSCHRHPLLPD | NMWSSORFQAHLQEMGAPNAWST | |
| HOTTTL | (103) | --VHLCNNSIQKHLENSCHRHPLLPD | NMWSSORFQAHLQEMGAPNAWST | |
| | | 301 | | 350 |
| BGS-42 | (283) | VIYPSMKKAIAHAMKVAQDHVEPRKN-- | SFELYGADFVLEGRDFRPWLIE | |
| TTL_PIG | (282) | SILLQIKHIIRSCLLSVEPAISTRELPHYQ | SFQLEGFDFMVEDEKVPWLIE | |
| TTLH_Hu | (280) | KLEDETHWIVQSLKAVAPVMNNDKH-- | CFECYGYDTITDDKLKPWLIE | |
| TTLH_Hu | (211) | ITVPGMKDAVIHALQTSQDTVQCRKA-- | SFELYGADFVLEGEDFQPWLIE | |
| HOTTTL | (151) | ITVPGMKDAVIHALQTSQDTVQCRKA-- | SFELYGADFVLEGEDFQPWLIE | |

6/24

FIG. 3B

| | | | | |
|---------|-------|--|-------|-------------|
| | | 351 | | 400 |
| BGS-42 | (330) | INSSPTMHPSTPVTAQLCAQVQEDTIKVAMD | ----- | RSCDIG |
| TTL_PIG | (332) | VNG-----APACAQKLYAELCOGIVDIATAS | ----- | |
| TTLH_Hu | (327) | VNASPSLTSSTANDRIKYNLIINDTLNIAMPNGEIPDCKWNKSPPKEVLG | | |
| TTLH_Hu | (258) | INASPTMAPSTAVTARLCAGVQADTLRVVIDR | ----- | MLDRNC DTG |
| HOTTL | (198) | INASPTMAPSTAVTARLCAGVQADTLRVVIDR | ----- | MLDRNC DTG |
| | | 401 | | 450 |
| BGS-42 | (367) | NFELLWRQPVVEPPFSGSDLGVAGVSVRRARQVLPVCNLKASASLLDA | | |
| TTL_PIG | (358) | VFPPPDAAEQQQQ-----OPPPAAFTKL | ----- | |
| TTLH_Hu | (377) | NYEELLYDEELAQGDGADRELRSRQGQSLGPRAGR | ----- | SRDSGRAVLTT |
| TTLH_Hu | (299) | AFELIYKQPVTTSFASTPRPSCLIPMYSDTRAR | ----- | SSDDSTASW |
| HOTTL | (239) | AFELIYKQPVTTSFASTPRPSCLIPMYSDTRAR | ----- | SSDDSTASW |
| | | 451 | | 500 |
| BGS-42 | (417) | QPLKARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESG | | |
| TTL_PIG | (380) | ----- | | |
| TTLH_Hu | (422) | WK----- | | |
| TTLH_Hu | (341) | WALRPCRPOARP | ----- | |
| HOTTL | (281) | WALRPCRPOARP | ----- | |
| | | 501 | | 550 |
| BGS-42 | (467) | GAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAH | | |
| TTL_PIG | (380) | ----- | | |
| TTLH_Hu | (424) | ----- | | |
| TTLH_Hu | (353) | ----- | | |
| HOTTL | (293) | ----- | | |
| | | 551 | | 575 |
| BGS-42 | (517) | PLEPVLRLGLKTAEGALRPPPGGKGS | | |
| TTL_PIG | (380) | ----- | | |
| TTLH_Hu | (424) | ----- | | |
| TTLH_Hu | (353) | ----- | | |
| HOTTL | (293) | ----- | | |

7/24

FIG. 4

| Model | Description | Score | E-value | N |
|-------|---|-------|---------|------|
| ----- | ----- | ----- | ----- | ---- |
| TTL | Tubulin-tyrosine ligase family | 293.0 | 3.7e-84 | 1 |
| Q | 73 EDIDTS----ADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSR-----NYFSQCQALL ++ID + +++ ++ + W ++ ++ ++ + + ++ +++++ | | | |
| T | 1 MRIDMHYRMMHQMINHFPGSYWITRKDRLWMNIKRMMCDFHWKHDHFDWMPRTFILPTDY | | | |
| Q | 122 NRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMRVEEILELAA----ADHPLSRDN +++ + ++ + +G++N+WI+KP++++RGR+I++M+ ++I+ ++ +P++ ++ | | | |
| T | 61 QEFVDYWQKHEWWGQDNHWIVKPWNSCRGRGIWIMNDWKQIPRWVNDFMDNPFVFPQHQR | | | |
| Q | 177 KWVVQKYIETPLLICD-----TKFDIRQWFLVTDWNPLTIWIFYKESYLRFS--LD +WVVQKYIE PLLI +KFDIR+++LVT++NPL+I++Y+E+++RF+++ ++ + | | | |
| T | 121 PWVVQKYIERPLLDGMDVGHKKFDIRCYVLVTSFNPLRIYVYREGWCRFCSVKYHPMDN | | | |
| Q | 230 KLDSAIHLCNNAVQKYLKN--DVGRSPLLPAHNMTSTRFQEYLQR--QGRGAVWGSVIY + +HL+N+++QK+ +N +R ++++ ++MWT +F++Y+++ + ++W +++ | | | |
| T | 181 FDNYCMHLTNYCIQKHYSNYSRCNRDYNCHGHMWTLQNFWNYYENMGIDWDNIWSQICD | | | |
| Q | 286 PSMKKAIAHA-MKVAQDHVEPRKNSFELYGADFVL---GRDFRPWLIEINSSPTMHPST + +K+++A++ +++++++PR+N+FELYG+DF + +++ PWL+E+N+SP+MH+++ | | | |
| T | 241 IIIKTIVAACVEACRMNMQPRYNCFELYGFDFMIQWDDDENLKPWLLEVNWSPDMHCTC | | | |
| Q | 341 PVTAQLCAQVQEDTIK-----VAVDRSCDI P+++ LC+Q+++D+++ V +D++ D+ | | | |
| T | 301 PYDMHLCHQLIRDVLNCAGCHVPPDCMKDC | | | |

8/24

FIG. 5A

BGS-42 – Clone A

TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGGAAGTGGGGCGGGTTGG
GGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGAT
AGGGCGAGGCTGTGCTGTCTTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGC
ATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAG
CCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCAAGA
TGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGACAT
CGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCGA
CACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGAC
CCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTTCATCTCCAATTCAAGAAATT
ACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGAC
GGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCG
GGGCCGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTC
ATCTGTGACACCAAGTTCGACATCAGACAGTGGTTTCCTCGTCACGGACTGGAACC
CCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTT
CTCCCTGGACAAGCTGGACAGCGCCATCCACCTGTGCAACAACACCGTCCAGAA
GTACCTGAAGAATGATGTGGGCCGCAGCCCCCTGCTGCCCCGCACACAACATGTG
GACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTG
GGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCACGCCATGAAGGT
GGCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGA
CTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCC
ACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAG
GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTC
CTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCCATTACAGCGGGTCCGACCTCTGCG
TGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCCGTCTGCAACC
TCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCT
CGGCCATGCCAGACCCTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTT
GGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGCTGGCACCCCTTAAGGGG
GGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAA
GGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCCAAACAC
CGGTGTCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGA
GCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCG
TCCGCCGCCCCGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCAGGAG
TACAGGTTGCAGCCACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGT
CTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAG
CTGTCAGTTCTATCTGCCAGCTTTTGAGTGTTCATTTGATTTTACTTATTCAACC
TGGAATTTGAATGTCAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:9)

9/24

FIG. 5B

BGS-42 – Clone B

GTAGCAGCGTGGGAAGAAGGAGTTCCTGGAAGACTTCCGGCGCACCATGGGCATC
CAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAG
CAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGC
AAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGG
ACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACA
TCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACC
TGACCCAGCAGTACTACTCCCTCGTTCATGCCAGGCTCTGCTGAATAGAATCACG
TCTGTGAACCCTCAGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGC
CCGCGGCCAAGTCCCGGGGCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGA
TCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACAACAAGTGGGTGGT
CCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCGACATCAG
ACAGTGGTTCCTCGTCACGGACTGGAACCCCCCTGACCATCTGGTTCTACAAGGAG
AGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCA
TCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCA
GCCCCCTGCTGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCT
GCAGCGCCAGGGCCGCTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAA
GAAGGCCATCGCCACGCCATGAAGGTGGCCAGGACCACGTGGAGCCTCGCAA
GAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCC
TGGCTGATCGAGATCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGG
CCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCA
GCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGCCGGTGGTTGAGCCGCCCCCA
TTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAAGTGTGAGGAGAGCCAGGAGG
CAGGTGCTGCCCCGTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGC
CGCTGAAGGCACGGGGCCCCCTCGGCCATGCCAGACCCTGCCCAGGGACCCCCAT
CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGGCTCCCCCTGG
CCTTGCTGGCACCCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCA
CCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGT
GGACAGTCAGGCCCCAAACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTG
GGATCCAAACCAGCTAAATGAGCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAA
GACAGCAGAGGGCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTTCATGACAGCG
TCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCCACTCTCCCGCCGAACATTGA
ATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTC
AGCCATCACTCTCCAAGGGGAGCTGTCAAGTTCTATCTGCCAGCTTTTGAGTGTTT
AATTTGATTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAAAAAAAAAA
AAAAAAAAA (SEQ ID NO:10)

10/24

FIG. 5C

BGS-42 – Clone C

CCCAGGACTCCTGGTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCACCC
CCAGCACCCCTGTGCCCTTTGCTCTGTGTCTCTGGGTGAATCCGGGGGCCCCAGAA
GCTCCCTCCTCAGGGCACAGAGGCCAAAGATGGGGCTGACTGGGGGCTGCCACC
GGGCTTTGGGTGCTGAGGGGGCTGTGGGACCCAGGGGAAGAGGTGCCGCTCCC
CCCAGCACCGGGCACTCCCCCGCCTCCCCCGGCCTCCAGCCCTGCACAAAGCAGC
TTGCCACACCCTTCCCACCAAGGCCCAGGGCTGAGGCCTGCCCAGGACGCAGGG
TGTGGGGACCCTGCTGAGGGAGGGGTCCCGGAAGAGGGGCTTCCCTGGCACAGA
GGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAGGT
GCAGGACAAGGTTCCCTTCCGCACCTAATAACCCAGGGTCAGGCCAGCGCCAGC
GCTGCTAGTGGCAACATGGCCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGC
GTGCGCTGTGTTTTCTGGGGGCCAGCCACTTTTTTCTTAACGGGGTGACAAACC
AGACATCGGGGTGCGGGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCT
CGCGTGTGGTGGGCAGTGCTGGGCATGTGGCTGCGTTCCGGGGCCCTGCAGCCGCT
CCTCCCTCTCCTGGGGTCTGAGGTGTGGGACACCCTGTGGCCCGTTTGGGGGCCT
GGAGGGAGCCCCAGTGCCACCGCCCTCGGTGCCCTCAGCTGCAGCCTCCCCATT
CCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGGATGCGTCTGAGCCTGGCCTG
CACATCCATGCTCCCACCGGCTGGAGGGGGTGTCTGGGGCCCTGGGGGACCGT
ATATCTGGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTGCCCCATAG
CCAGGCAAGTCTGAGGTGGACGGCCCGTCCCTCGCCTTGTGAGCGAGGCAGAGCT
GAGCTGAGCTGCCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTG
CGTGAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCCGACTCCTTCTC
CCACGCTGCTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAG
TGAGGAGACGGCAGAGGGGCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGAT
CCCCCTGGTGCTGAGACAGACTGATGGGGCAGGGTCTGAGGATAGAGGACCGGG
GAGAGGCCTCCCATGGTCATGGTCATGGCAGTACAGAGGCCAGGGGGCCCCGGGA
GGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTCTGTGCTAGGCTTGTGGACAGCG
CGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTTCGGAGGCCGAGGGGTGCAGC
TGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGCAGACTGGGG
GTGTGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGT
TGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCCTGGCTCGGACA
GATAGGGCGAGGCTGTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCC
AGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGC
AAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCA
AGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGA
CATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACAT
CGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCT
GACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGA
AATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC
AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGT
CCCGGGGCGGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCT
GCTCATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGG
AACCCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGC
GCTTCTCCCTGGACAAG

11/24

FIG. 5C (CONT.)

CTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAA
GAATGATGTGGGCCGCGAGCCCCCTGCTGCCCGCACACAACATGTGGACCAGCAC
CAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGT
CATCTACCCGTCCATGAAGAAGGCCATCGCCACGCCATGAAGGTGGCCCAGGA
CCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCCTT
GGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCATGCAC
CCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATC
AAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGG
CAGCCGGTGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCGTGGCGGGCG
TCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCT
CGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCCTCGGCCATGC
CAGACCCTGCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGA
AGGAAGAGAAGGGGCTCCCCCTGGCCTTGCTGGCACCCCTTAAGGGGGGCAGCCG
AGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGC
TCCCGGCCTGCCCTGTGCGCCACGTGGACAGTCAGGCCCCAAACACCGGTGTCCC
CGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGCACCCGCT
GGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGCC
CGGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTG
CAGCCACTCTCCCGCCGAACATTGAATACGTCTTCCACCATCTTGTCTTTGCTGT
GGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGT
TCTATCTGCCAGCTTTTGAGTGTTCATTTGATTTTACTTATTCAACCTGGAATTT
GAATGTCAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:11)

12/24

FIG. 6A

1 GTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCACCCACAGCACCCCTGTGCCCT 60
61 TTGCTCTGTGTCTCTGGGTGAATCCGGGGCCCCAGAAGCTCCCTCCTCAGGGCACAGAGG 120
121 CCAAAGATGGGGCTGACTGGGGGCTGCCACCGGGCTTTGGGTGCTGAGGGGGCTGTGGGA 180
181 CCCCAGGGGAAGAGGTGCCGCTCCCCCAGCACCGGGCACTCCCCGCCTCCCCGGCCT 240
241 CCAGCCCTGCACAAAGCAGCTTGCCACACCCTTCCCACCAAGGCCCAGGGCTGAGGCCTG 300
301 CCCAGGACGCAGGGTGTGGGGACCCTGCTGAGGGAGGGTCCCGGAAGAGGGCTTCCCT 360
361 GGCACAGAGGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAG 420
421 GTGCAGGACAAGGTTCCCTTCCGCACCTAATACCCAGGGTCAGGCCAGCGCCAGCGCTG 480
481 CTAGTGGCAACATGGCCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGCGTGCCTGTG 540
541 TTTTCTGGGGGCCAGCCACTTTTTCTTAACGGGGTGACAAACCAGACATCGGGGTGCG 600
601 GGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCTCGCGTGTGGTGGGCAGTGCT 660
661 GGGCATGTGGCTGCGTTCCGGGCCCTGCAGCCGCTCCTCCCTCTCCTGGGGTCTGAGGTG 720
721 TGGGACACCCTGTGGCCCGTTTGGGGGCTGGAGGGAGCCCCAGTGCCACCGCCCTCGG 780
781 TGCCCTCAGCTGCAGCCTCCCCATTCCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGG 840
841 ATGCGTCTGAGCCTGGCCTGCACATCCATGCTCCCACCGGCTGGAGGGGTGTTCTGGGG 900
901 CCCTGGGGGACCGTATATCTGGGGAGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTG 960
961 CCCCATAGCCAGGCAAGTCTGAGGTGGACGGCCCGTCCTCGCCTTGTGAGCGAGGCAGAG 1020
1021 CTGAGCTGAGCTGCCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTGCGT 1080
1081 GAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCGACTCCTTCTTCCCACGCTG 1140

13/24

FIG. 6B

| | | |
|------|--|------|
| 1141 | CTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAGTGAGGAGACGGCAG | 1200 |
| 1201 | AGGGCCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGATCCCCCTGGTGCTGAGACAGA | 1260 |
| 1261 | CTGATGGGGCAGGGTCTGAGGATAGAGGACCGGGGAGAGGCCTCCCATGGTCATGGTCAT | 1320 |
| 1321 | GGCAGTACAGAGGCCAGGGGCCCCGGGAGGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTC | 1380 |
| 1381 | TGTGCTAGGCTTGTGGACAGCGCGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTCGGA | 1440 |
| 1441 | GGCCGAGGGGTGCAGCTGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGC | 1500 |
| 1501 | AGACTGGGGGTGTGGGAGCAGGCCTGGGCCCATCGGCTATGAGGGCGGGAAGTGGGGCG | 1560 |
| 1561 | GGTTGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGA | 1620 |
| 1621 | TAGGGCGAGGCTGTGCTGTCTTTTCAGAGTAGCAGCGTGGGAAGAAGGAGTTCCTGGAAG | 1680 |
| 1681 | ACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCA | 1740 |
| 1 | M A S S I L K W V V S H Q S C S | 16 |
| 1741 | GCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGA | 1800 |
| 17 | R S S R S K P R D Q R E E A G S S D L S | 36 |
| 1801 | GCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGCAGCTTG | 1860 |
| 37 | S R Q D A E N A E A K L R G L P G Q L V | 56 |
| 1861 | TGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCG | 1920 |
| 57 | D I A C K V C Q A Y L G Q L E H E D I D | 76 |
| 1921 | ACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGACCCAGC | 1980 |
| 77 | T S A D A V E D L T E A E W E D L T Q Q | 96 |
| 1981 | AGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGAAATTACTTTTCGC | 2040 |
| 97 | Y Y S L V H G D A F I S N S R N Y F S Q | 116 |
| 2041 | AGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGACGGACATTGACGGGC | 2100 |
| 117 | C Q A L L N R I T S V N P Q T D I D G L | 136 |

FIG. 6C

| | | |
|------|---|------|
| 2101 | TCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCCGAGACATAGTGTGCA | 2160 |
| 137 | R N I W I I K P A A K S R G R D I V C M | 156 |
| 2161 | TGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACA | 2220 |
| 157 | D R V E E I L E L A A A D H P L S R D N | 176 |
| 2221 | ACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCG | 2280 |
| 177 | K W V V Q K Y I E T P L L I C D T K F D | 196 |
| 2281 | ACATCAGACAGTGGTTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGGTTCTACAAGG | 2340 |
| 197 | I R Q W F L V T D W N P L T I W F Y K E | 216 |
| 2341 | AGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCATCC | 2400 |
| 217 | S Y L R F S T Q R F S L D K L D S A I H | 236 |
| 2401 | ACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCGAGCCCCCTGC | 2460 |
| 237 | L C N N A V Q K Y L K N D V G R S P L L | 256 |
| 2461 | TGCCCCGACACAACATGTGGACCAGCACCAGTTCCAGGAGTACCTGCAGCGCCAGGGCC | 2520 |
| 257 | P A H N M W T S T R F Q E Y L Q R Q G R | 276 |
| 2521 | GTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCA | 2580 |
| 277 | G A V W G S V I Y P S M K K A I A H A M | 296 |
| 2581 | TGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTG | 2640 |
| 297 | K V A Q D H V E P R K N S F E L Y G A D | 316 |
| 2641 | ACTTCGTCTTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCA | 2700 |
| 317 | F V L G R D F R P W L I E I N S S P T M | 336 |
| 2701 | TGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCA | 2760 |
| 337 | H P S T P V T A Q L C A Q V Q E D T I K | 356 |
| 2761 | AGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGGCAGCCGG | 2820 |
| 357 | V A V D R S C D I G N F E L L W R Q P V | 376 |
| 2821 | TGGTTGAGCCGCCCCATTACAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGA | 2880 |
| 377 | V E P P P F S G S D L C V A G V S V R R | 396 |
| 2881 | GAGCCAGGAGGCAGGTGCTGCCCCGTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACG | 2940 |
| 397 | A R R Q V L P V C N L K A S A S L L D A | 416 |

15/24

FIG. 6D

| | | |
|------|---|------|
| 2941 | CGCAGCCGCTGAAGGCACGGGGCCCCTCGGCCATGCCAGACCCTGCCAGGGACCCCCAT | 3000 |
| 417 | Q P L K A R G P S A M P D P A Q G P P S | 436 |
| 3001 | CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGC | 3060 |
| 437 | P A L Q R D L G L K E E K G L P L A L L | 456 |
| 3061 | TGGCACCCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAG | 3120 |
| 457 | A P L R G A A E S G G A A Q P T R T K A | 476 |
| 3121 | CTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCTGTGCGCCACGTGGACAGTCAGGCCCCAA | 3180 |
| 477 | A G K V E L P A C P C R H V D S Q A P N | 496 |
| 3181 | ACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGC | 3240 |
| 497 | T G V P V A Q P A K S W D P N Q L N E H | 516 |
| 3241 | ACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGC | 3300 |
| 517 | P L E P V L R S L K T A E G A L R P P P | 536 |
| 3301 | CCGGAGGAAAAGGTTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCC | 3360 |
| 537 | G G K G S | 541 |
| 3361 | ACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGG | 3420 |
| 3421 | AAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGTTCTATCTGCCAGCTT | 3480 |
| 3481 | TTGAGTGTTCAATTTGATTTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAA | 3540 |
| 3541 | AAAAAAAAAAAAA | 3554 |

16/24

FIG. 7A

-2057 tgctgcagcagagcccggctgggatcctcacgctgcacgccatttgcctctgatggtt -1998
 -1997 gcctcactccatcccatcctggctggtgtgaaccttgaatgctgggcatcaataaagact -1938
 -1937 tttttcttgccagtctaggttggtaaaaaatgagatgccgtacctcctctggaccatcaa -1878
 -1877 gagggacatcattgactatcacagcctgacctacgaccagatgctgaaccactacgcaaa -1818
 -1817 gacagcctccttcaccaccaaggtgagccggccgcgcttgagcgtggcgggagccggcaa -1758
 -1757 gggtggtggggaggagcttctgcagccattagggaccctcggtggctggtcagtggccac -1698
 -1697 cagtcacctcctgggtgcatcccaggactcctggtctaaggccgtggccagaatcactcg -1638
 -1637 gtgcccacccccacccccagcaccctgtgccctttgctctgtgtctctgggtgaatccgg -1578
 -1577 ggccccagaagctccctcctcagggcacagaggccaaagatggggctgactgggggctgc -1518
 -1517 caccgggctttgggtgctgagggggctgtgggaccccaggggaagaggtgccgctcccc -1458
 -1457 cagcaccgggcaactccccgcctccccggcctccagccctgcacaaagcagcttgccac -1398
 -1397 acccttcccaccaaggcccagggtgaggcctgccaggacgcagggtgtggggaccctg -1338
 -1337 ctgagggaggggtcccgaagaggggcttccctggcacagaggtccctctcagcaggcca -1278
 -1277 ggtgcggtgcctcagcacagtgtggggcggaggtgcaggacaaggttcccttccgcacc -1218
 -1217 taataccccagggtcaggccagcgcctgctagtggcaacatggcccttcaaaga -1158
 -1157 ccccgtgtgcagagccagtcagcgtgcgctgtgttttctgggggcccagccactttttcc -1098
 -1097 ttaacaggggtgacaaaaccagacatcgggggtgcggggacttcacgatatgcctctctaag -1038
 -1037 gcgcgtgctacctcgctgtggtggccagtgcctggcatgtggctgcgttccgggacctg -978
 -977 cagccgctcctccctctcctggggtctgaggtgtgggacaccctgtggcccggtttggggg -918
 -917 cctggagggagccccagtgcccaccgcctcggtgcctcagctgcagcctccccattcc -858

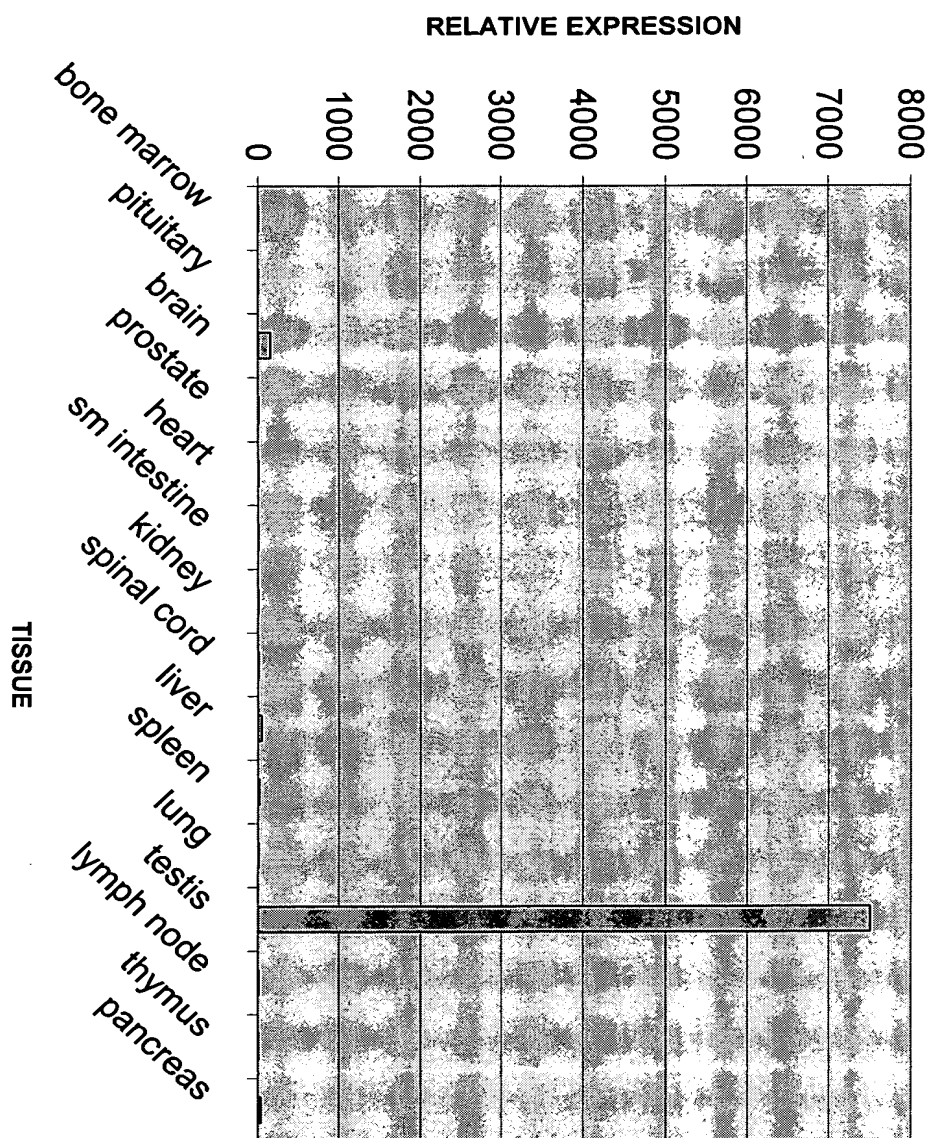
17/24

FIG. 7B

| | | |
|------|---|------|
| -857 | ctggggcctgccacgccctccactgcctcaaggatgcgtctgagcctggcctgcacatcc | -798 |
| -797 | atgctcccaccggctggaggggtgttcttggggccctgggggaccgtatatctggggagg | -738 |
| -737 | gggagggatccgccctaggggtgctgtgtggtgccccatagccaggcaagtctgaggtgg | -678 |
| -677 | acggcccgtcctcgcccttgtgagcgaggcagagctgagctgagctgcccctcctgcctaa | -618 |
| -617 | cacgccactgtctctggagatcgggctgtgcgtgaacatgcggagcctgccctggtacgt | -558 |
| -557 | cccgcccaaccccgactccttcttcccacgctgctacagcctctgcaccgagagtggca | -498 |
| -497 | gcaggagttcctgggtaagtgaggagacggcagagggccccagtgctgtcagcagagagg | -438 |
| -437 | cttctagaaagatccccctggtgctgagacagactgatggggcagggctctgaggatagag | -378 |
| -377 | gaccggggagaggcctcccatggtcatggtcatggcagtagagggccaggggccccggg | -318 |
| -317 | agggagggcgggcagtcaggagtggtgtgtgttctgtgctaggcttgtggacagcgggcg | -258 |
| -257 | agcagctggggcaaggccggctccgtggtcggaggccgaggggtgcagctggacggccgc | -198 |
| -197 | agtcacagagacactgcagggagaagggcaggcagactgggggtgtgggagcaggcctgg | -138 |
| -137 | gccccatcggtatgagggcggggaagtggggcggggtggggagcctccgtggccctggcc | -78 |
| -77 | ccatctccagtcccagtcctggctcggacagatagggcgaggctgtgctgtcctttcag | -18 |
| -17 | aagacttcggcgccaccatggcatccagcatcctcaagtgggtggtcagccaccagagct | 42 |
| 1 | M A S S I L K W V V S H Q S C | 15 |
| 43 | gcagcaggagcagcagaagcaagcccagggaccagagggaggaggccgggagcagcgacc | 102 |
| 16 | S R S S R S K P R D Q R E E A G S S D L | 35 |
| 103 | tgagcagcaggcaaggtgcgctgggccggggcagggcagtgccaggccaccagagctcgg | 162 |
| 36 | S S R Q G A L G R G R A V P G H Q S S G | 55 |
| 163 | ggcctccacaggggccctccc | 183 |
| 56 | P P Q G P S | 61 |

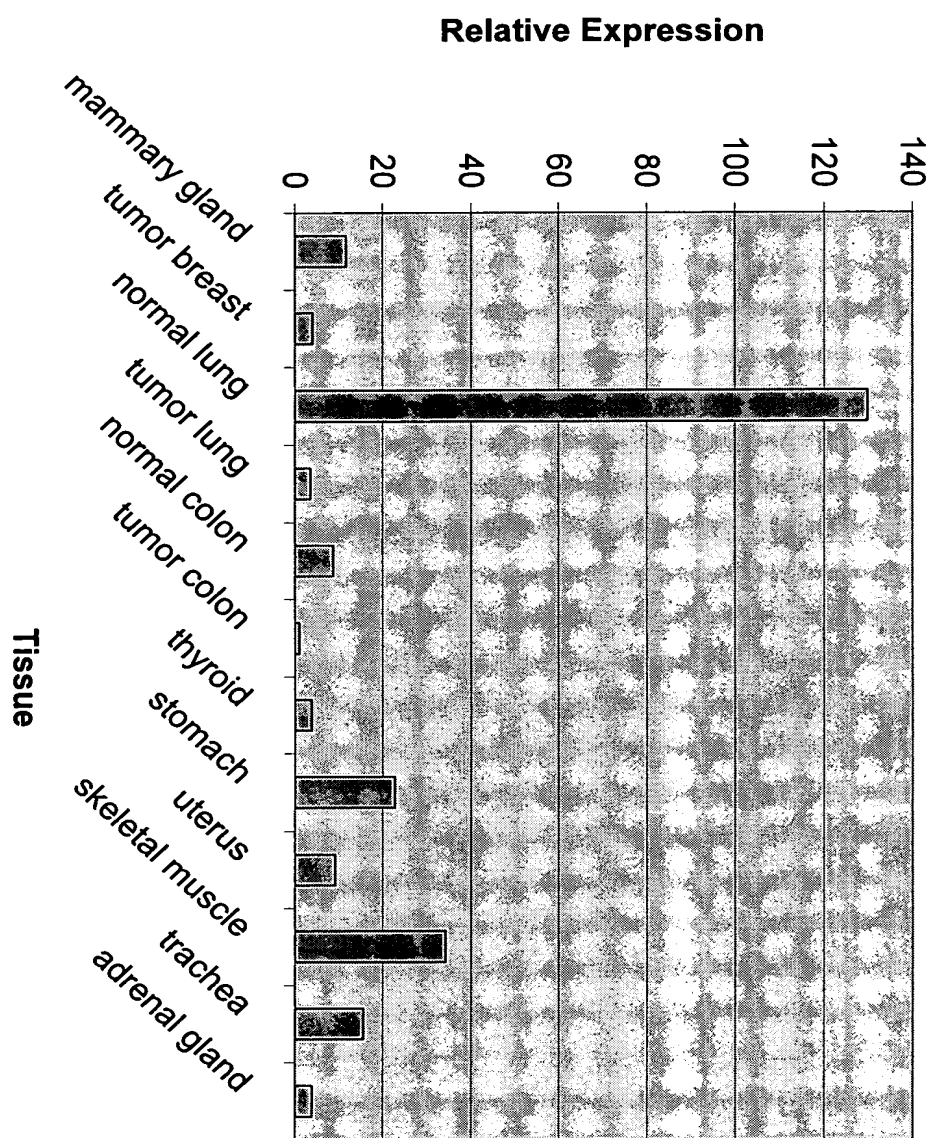
18/24

FIG. 8



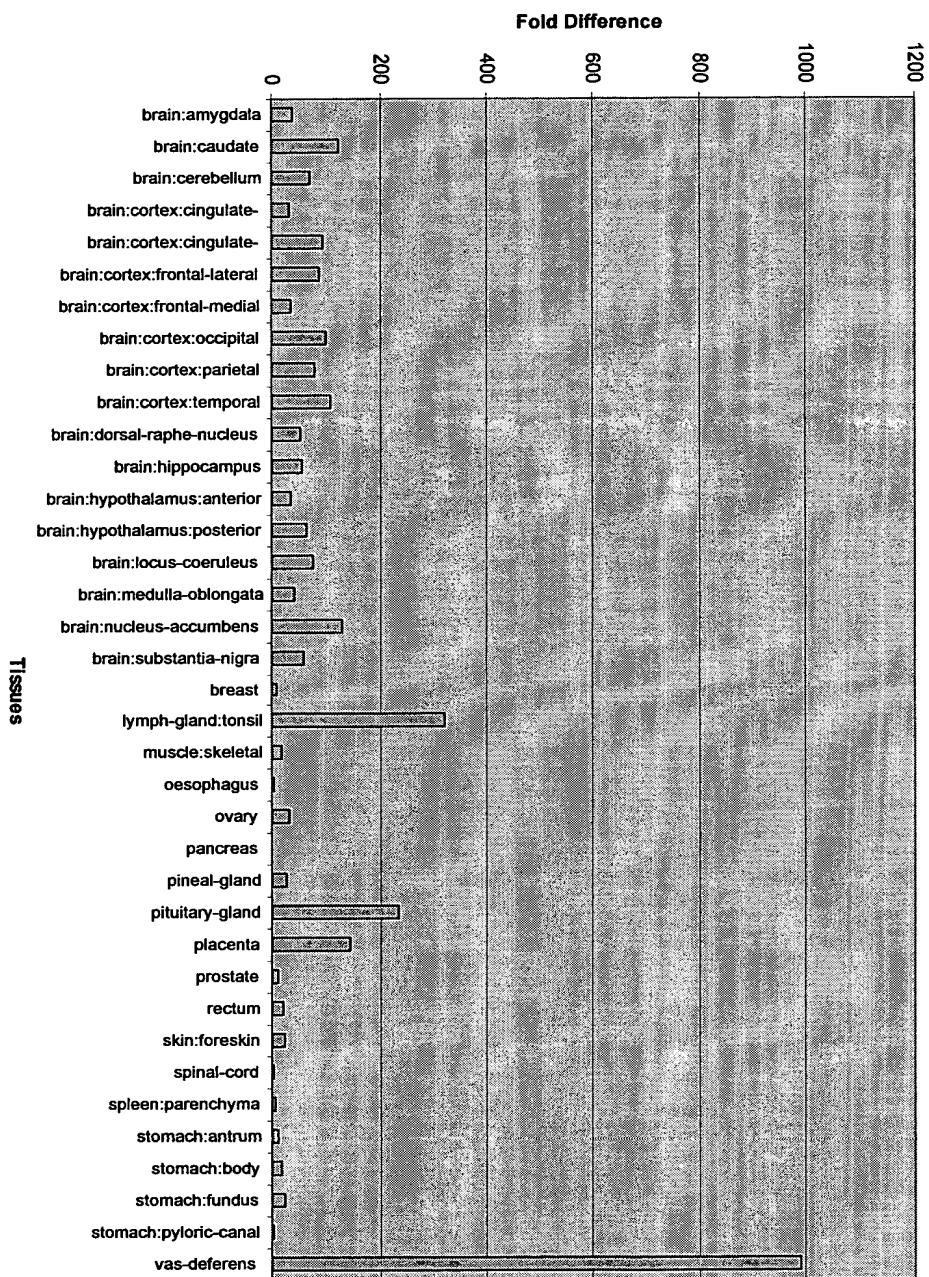
19/24

FIG. 9



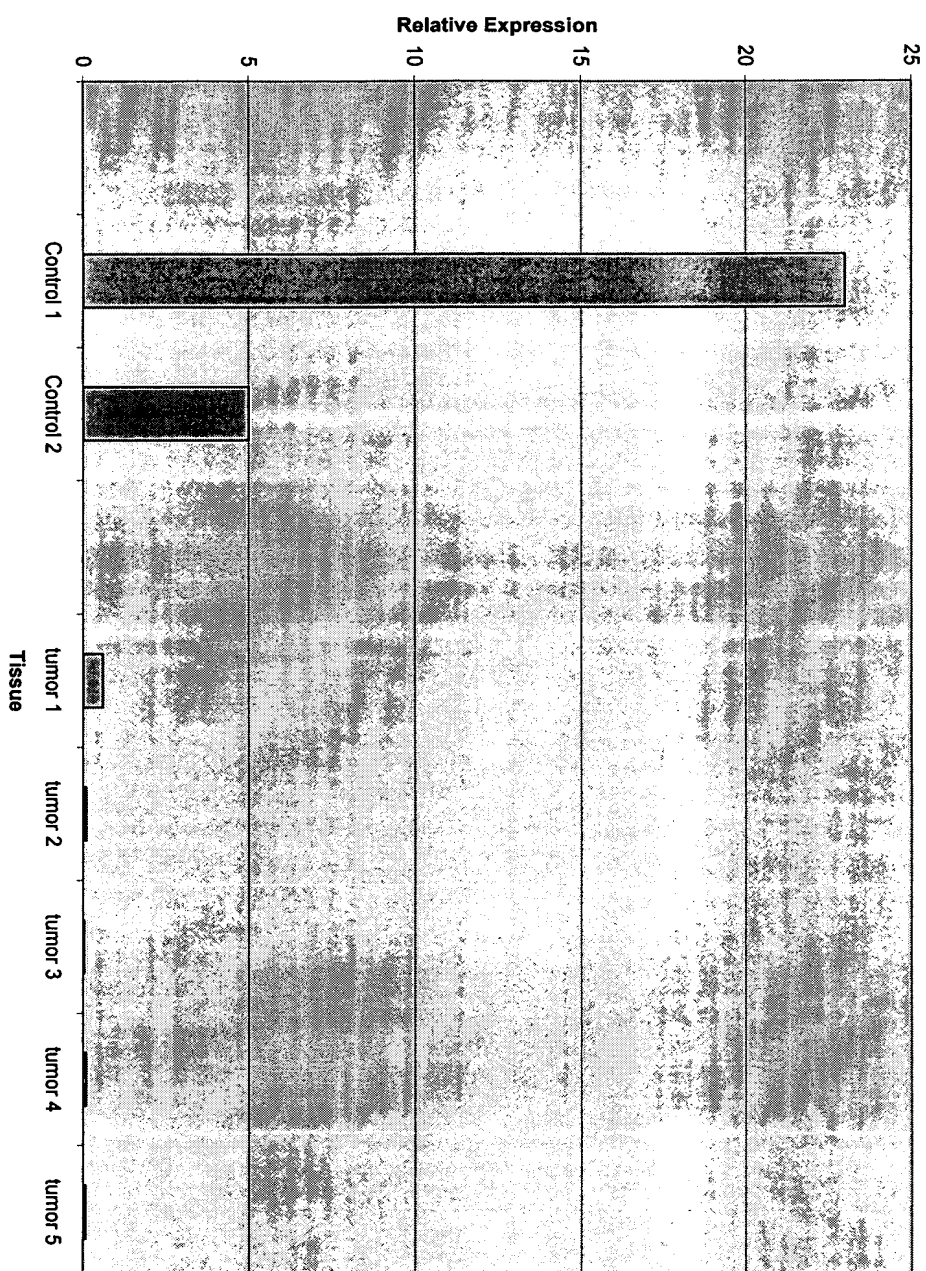
20/24

FIG. 10



21/24

FIG. 11



22/24

FIG. 12

| Protein | Genbank ID | Identities | Similarities |
|---|-------------|------------|--------------|
| Human HOTTL protein | gi 6683745 | 57.5% | 65.5% |
| Pig tubulin--tyrosine ligase protein (TTL) | gi 423218 | 29.4% | 40.0% |
| Human tubulin tyrosine ligase-like protein (TTLH_HUMAN) | gi 20455371 | 53.3% | 61.4% |
| Human tubulin tyrosine ligase-like protein (TTLL_HUMAN) | gi 20455347 | 27.4% | 38.4% |

23/24

FIG. 13

| | | | | | |
|-------|------------|-------------|------------|------------|-------------|
| 1gsaA | MIKLGIVMDP | IANINIKKDS | SFAMLLAQ | RGYELHYMEM | GDLYLINGEA |
| BGS42 | |MAS | SILKWVSHQ | SCSRSSRSKP | RDQREEAGSS |
| | | | | | |
| 1gsaA | RAHTRTLNVK | QNYEEWFSFV | GEQDLPLADL | DVILMRKDPP | FDTEFIYATY |
| BGS42 | DLSSRQDA.. | ENAEAKLRGL | PGQLVDIACK | VCQAYLGQLE | HEDIDTSADA |
| | | | | | |
| 1gsaA | ILERAEEKGT | LIVNKPQSLR | DCNEKLFTAW | FSDLTPETLV | TRNKAQLKAF |
| BGS42 | VEDLTEAEWE | DLTQQYYSLV | HGDAFISNSR | NYFSQCQALL | NRITSVNPQT |
| | | | | | |
| | | ^* ^* | * * | | ^^* |
| 1gsaA | WEKHS..DII | LKPLDGMGGA | SIFRVKEGDP | NLGVIAETLT | EHGTRYCMAQ |
| BGS42 | DIDGLRNIWI | IKPAAKSRGR | DIVCMDRVEE | ILELAAADHP | LSRDNKWVVQ |
| | ** | * | ^ ^ | | |
| | | | | | |
| 1gsaA | NYLPAIKDG. |DKRVLV | VDGEPVPYCL | ARIP..... | |
| BGS42 | KYIETPLLIC | DTKFDIRQWF | LVTDWNPLTI | WFKESYLRF | STQRFSLDKL |
| | | | | | |
| 1gsaA | | | | .QGGETRGNL | AAGGRGEPRP |
| BGS42 | DSAIHLCNNA | VQKYLKNDVG | RSPLLPAHNM | WTSTRFQEYL | QRQGRGAVWG |
| | | | | | |
| | | | ^ | *^^ | ^* |
| 1gsaA | L..... | ..TESDWKIA | RQIGPTLKEK | GLIFVGLDII | GDR.....LT |
| BGS42 | SVIYPSMKKA | IAHAMKVAQD | HVEPRKNSFE | LYGA...DFV | LGRDFRPWLI |
| | | | | | |
| | *** | | | | |
| 1gsaA | EINVTSPTCI | REIEAEFPVS | ITGMLMDAIE | ARLQ..... | |
| BGS42 | EINSSPTMHP | STPVTAQLCA | QVQEDTIKV. | AVDRSCDIGN | FELLWRQPVV |
| | | | | | |
| 1gsaA | | | | | |
| BGS42 | EPPPFSGSDL | CVAGVSVRRA | RRQVLPVCNL | KASASLLDAQ | PLKARGPSAM |
| | | | | | |
| 1gsaA | | | | | |
| BGS42 | PDPAQGPPSP | ALQRDGLGLKE | EKGLPLALLA | PLRGAAESGG | AAQPTRTKAA |
| | | | | | |
| 1gsaA | | | | | |
| BGS42 | GKVELPACPC | RHVDSQAPNT | GVPVAQPAKS | WDPNQLNAHP | LEPVLRLGLKT |
| | | | | | |
| 1gsaA | | | | | |
| BGS42 | AEGALRPPPG | GKGS..... | | | |

FIG. 14

